

RAW SEQUENCE LISTING

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Application Serial Number: 10/828,975
Source: 1FW9
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DATE: 02/25/2005

PATENT APPLICATION: US/10/828,975

TIME: 15:14:36

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Output Set: N:\CRF4\02252005\J828975.raw

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3 <110> APPLICANT: REN, DEJIAN
4     CLAPHAM, DAVID E.
5     GARBERS, DAVID L.
6     QUILL, TIMOTHY A.
8 <120> TITLE OF INVENTION: SPERM-SPECIFIC CATION CHANNEL, CATSPER2, AND USES
9     THEREFOR
11 <130> FILE REFERENCE: 110313.136US2
13 <140> CURRENT APPLICATION NUMBER: 10/828,975
14 <141> CURRENT FILING DATE: 2004-04-21
16 <150> PRIOR APPLICATION NUMBER: PCT/US02/33676
17 <151> PRIOR FILING DATE: 2002-10-22
19 <150> PRIOR APPLICATION NUMBER: 60/345,324
20 <151> PRIOR FILING DATE: 2001-10-22
22 <160> NUMBER OF SEQ ID NOS: 7
24 <170> SOFTWARE: PatentIn Ver. 3.3
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27 <211> LENGTH: 1587
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 cggcacacta tcagggagtt acttgatcct tcccgccaga agaaacttgt attgggagat 180
35 caacaccagc tagtgcggtt ctctataaag cctcagcgta tagaacagat ttcacatgcc 240
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37 gcgggatggg tccttgagtg tcctctcttc aaaaacttca tcatcttctt ggtctttttg 360
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39 ccattgaagc tgaccttgga ggtggcagct tgggttatct tgcttatttt catcctggag 480
40 atccttctta agtggctatc caacttttct gttttctgga agagtgcctg gaatgtcttt 540
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43 cttgcacaat tccgtcaaat tcaaattatt attttggtcc tggtcagggc cctcaagagc 720
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56 gaaatggatc aggatgaccg tgtttggccc agagactcac tcttcgata ttttgagttg 1500
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71 20 25 30
73 Gln Gly Leu Ser Gln Ala Val Pro Arg His Thr Ile Arg Glu Leu Leu
74 35 40 45
76 Asp Pro Ser Arg Gln Lys Lys Leu Val Leu Gly Asp Gln His Gln Leu
77 50 55 60
79 Val Arg Phe Ser Ile Lys Pro Gln Arg Ile Glu Gln Ile Ser His Ala
80 65 70 75 80
82 Gln Arg Leu Leu Ser Arg Leu His Val Arg Cys Ser Gln Arg Pro Pro
83 85 90 95
85 Leu Ser Leu Trp Ala Gly Trp Val Leu Glu Cys Pro Leu Phe Lys Asn
86 100 105 110
88 Phe Ile Ile Phe Leu Val Phe Leu Asn Thr Ile Ile Leu Met Val Glu
89 115 120 125
91 Ile Glu Leu Leu Glu Ser Thr Asn Thr Lys Leu Trp Pro Leu Lys Leu
92 130 135 140
94 Thr Leu Glu Val Ala Ala Trp Phe Ile Leu Leu Ile Phe Ile Leu Glu
95 145 150 155 160
97 Ile Leu Leu Lys Trp Leu Ser Asn Phe Ser Val Phe Trp Lys Ser Ala
98 165 170 175
100 Trp Asn Val Phe Asp Phe Val Val Thr Met Leu Ser Leu Leu Pro Glu
101 180 185 190
103 Val Val Val Leu Val Gly Val Thr Gly Gln Ser Val Trp Leu Gln Leu
104 195 200 205
106 Leu Arg Ile Cys Arg Val Leu Arg Ser Leu Lys Leu Leu Ala Gln Phe
107 210 215 220
109 Arg Gln Ile Gln Ile Ile Ile Leu Val Leu Val Arg Ala Leu Lys Ser
110 225 230 235 240
112 Met Thr Phe Leu Leu Met Leu Leu Leu Ile Phe Phe Tyr Ile Phe Ala
113 245 250 255
115 Val Thr Gly Val Tyr Val Phe Ser Glu Tyr Thr Arg Ser Pro Arg Gln
116 260 265 270
118 Asp Leu Glu Tyr His Val Phe Phe Ser Asp Leu Pro Asn Ser Leu Val
119 275 280 285
121 Thr Val Phe Ile Leu Phe Thr Leu Asp His Trp Tyr Ala Leu Leu Gln
122 290 295 300
124 Asp Val Trp Lys Val Pro Glu Val Ser Arg Ile Phe Ser Ser Ile Tyr
125 305 310 315 320

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133 Glu Glu Met Ala Arg Arg Glu Val Gln Leu Lys Ala Asp Met Phe Lys
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136 Arg Gln Ile Ile Gln Arg Arg Lys Asn Met Ser His Glu Ala Leu Thr
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139 Ser Ser His Ser Lys Ile Glu Asp Arg Gly Ala Ser Gln Gln Arg Glu
140 385           390           395           400
142 Ser Leu Asp Leu Ser Glu Val Ser Glu Val Glu Ser Asn Tyr Gly Ala
143           405           410           415
145 Thr Glu Glu Asp Leu Ile Thr Ser Ala Ser Lys Thr Glu Glu Thr Leu
146           420           425           430
148 Ser Lys Lys Arg Glu Tyr Gln Ser Ser Ser Cys Val Ser Ser Thr Ser
149           435           440           445
151 Ser Ser Tyr Ser Ser Ser Ser Ser Glu Ser Arg Phe Ser Glu Ser Ile Gly
152           450           455           460
154 Arg Leu Asp Trp Glu Thr Leu Val His Glu Asn Leu Pro Gly Leu Met
155 465           470           475           480
157 Glu Met Asp Gln Asp Asp Arg Val Trp Pro Arg Asp Ser Leu Phe Arg
158           485           490           495
160 Tyr Phe Glu Leu Leu Glu Lys Leu Gln Tyr Asn Leu Glu Glu Arg Lys
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171 <211> LENGTH: 1245
172 <212> TYPE: DNA
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178 cggcacacta tcagggagtt acttgatcct tcccgccaga agaaacttgt attgggagat 180
179 caacaccagc tagtgcgttt ctctataaag cctcagcgta tagaacagat ttcacatgcc 240
180 cagaggctgt tgagcagget tcatgtgcgc tgcagtcaga ggccacctct ttctttgtgg 300
181 gccggatggg tccttgagtg tcctctcttc aaaaacttca tcatcttctt ggtctttttg 360
182 aatacgatca tattgatggt tgaaatagaa ttgctggaat ccacaaatac caaactatgg 420
183 ccattgaagc tgaccttgga ggtggcagct tggtttatct tgcttatttt catcctggag 480
184 atccttctta agtggctatc caacttttct gttttctgga agagtgcctg gaatgtcttt 540
185 gactttgttg ttaccatggt gtccctgctt cccgagggtg tggattggt aggggtaaca 600
186 ggccaatcgg tgtggcttca gcttctgagg atctgccggg tgctgaggtc tctcaactc 660
187 cttgcacaat tccgtcaaat tcaaattatt attttgggtcc tggtcagggc cctcaagagc 720
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209 20 25 30
211 Gln Gly Leu Ser Gln Ala Val Pro Arg His Thr Ile Arg Glu Leu Leu
212 35 40 45
214 Asp Pro Ser Arg Gln Lys Lys Leu Val Leu Gly Asp Gln His Gln Leu
215 50 55 60
217 Val Arg Phe Ser Ile Lys Pro Gln Arg Ile Glu Gln Ile Ser His Ala
218 65 70 75 80
220 Gln Arg Leu Leu Ser Arg Leu His Val Arg Cys Ser Gln Arg Pro Pro
221 85 90 95
223 Leu Ser Leu Trp Ala Gly Trp Val Leu Glu Cys Pro Leu Phe Lys Asn
224 100 105 110
226 Phe Ile Ile Phe Leu Val Phe Leu Asn Thr Ile Ile Leu Met Val Glu
227 115 120 125
229 Ile Glu Leu Leu Glu Ser Thr Asn Thr Lys Leu Trp Pro Leu Lys Leu
230 130 135 140
232 Thr Leu Glu Val Ala Ala Trp Phe Ile Leu Leu Ile Phe Ile Leu Glu
233 145 150 155 160
235 Ile Leu Leu Lys Trp Leu Ser Asn Phe Ser Val Phe Trp Lys Ser Ala
236 165 170 175
238 Trp Asn Val Phe Asp Phe Val Val Thr Met Leu Ser Leu Leu Pro Glu
239 180 185 190
241 Val Val Val Leu Val Gly Val Thr Gly Gln Ser Val Trp Leu Gln Leu
242 195 200 205
244 Leu Arg Ile Cys Arg Val Leu Arg Ser Leu Lys Leu Leu Ala Gln Phe
245 210 215 220
247 Arg Gln Ile Gln Ile Ile Ile Leu Val Leu Val Arg Ala Leu Lys Ser
248 225 230 235 240
250 Met Thr Phe Leu Leu Met Leu Leu Leu Ile Phe Phe Tyr Ile Phe Ala
251 245 250 255
253 Val Thr Gly Val Tyr Val Phe Ser Glu Tyr Thr Arg Ser Pro Arg Gln
254 260 265 270
256 Asp Leu Glu Tyr His Val Phe Phe Ser Asp Leu Pro Asn Ser Leu Val
257 275 280 285
259 Thr Val Phe Ile Leu Phe Thr Leu Asp His Trp Tyr Ala Leu Leu Gln
260 290 295 300
262 Asp Val Trp Lys Val Pro Glu Val Ser Arg Ile Phe Ser Ser Ile Tyr
263 305 310 315 320
265 Phe Ile Leu Trp Leu Leu Leu Gly Ser Ile Ile Phe Arg Ser Ile Ile

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266          325          330          335
268 Val Ala Met Met Val Thr Asn Phe Gln Asn Ile Arg Lys Glu Leu Asn
269          340          345          350
271 Glu Glu Met Ala Arg Arg Glu Val Gln Leu Lys Ala Asp Met Phe Lys
272          355          360          365
274 Arg Gln Ile Ile Gln Arg Arg Lys Asn Met Ser His Glu Ala Leu Thr
275          370          375          380
277 Ser Ser His Ser Lys Ile Glu Asp Arg Ser Phe Gly Leu Gly Asp Ser
278 385          390          395          400
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281          405          410
284 <210> SEQ ID NO: 5
285 <211> LENGTH: 1767
286 <212> TYPE: DNA
287 <213> ORGANISM: Mus musculus
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292 actctccggg agatacttga tcttgcttac cagcagaaac tcatgtcagg agatcaggag 180
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315 aaagcctacc cagtttccca ttcaatctcg tcccatggct ccattgcagc cgatactgct 1560
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317 atggatcagg atgaccgcat tgtctggccc agagactcac tcttcggata ttctgagtta 1680
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323 <211> LENGTH: 588
324 <212> TYPE: PRT

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